<u>In the Specification:</u>

On page 1, please amend the "Related Application Information" paragraph (lines 7-10) as follows:

     <u>This application is a continuation of U.S. Application Serial No. 10/134,410, filed April 29, 2002, which</u> ~~This application~~ is a continuation-in-part of <u>U.S. A</u>[[a]]pplication <u>S</u>[[s]]erial <u>N</u>[[n]]umber <u>09/369,693, filed August 6, 1999</u> ~~09/131,263, filed August 7, 1998~~, [[and]] <u>which is a continuation-in-part</u> of <u>U.S. A</u>[[a]]pplication <u>S</u>[[s]]erial <u>N</u>[[n]]umber <u>09/131,263, filed August 7, 1998</u> ~~09/369,693, filed August 6, 1999~~, <u>all</u> [[both]] of which are hereby incorporated by reference <u>in their entirety</u>.

Please amend the paragraph on page 8, beginning on line 9, as follows:

     Figures 5A and 5B depict the cDNA sequence (SEQ ID NO:[[9]] <u>13</u>) of a human TANGO-93 clone that contains additional 3' untranslated sequence compared to SEQ ID NO:4. The open reading frame of SEQ ID NO:[[9]] <u>13</u> extends from nucleotide 63 to nucleotide 527. <u>The predicted amino acid sequence is also shown (SEQ ID NO:14).</u>

Please amend the paragraph on page 84, beginning on line 9, as follows:

     Additional analysis of human TANGO-93 clones provided additional 3' untranslated sequence. This longer cDNA sequence (SEQ ID NO:[[9]] <u>13</u>) is shown in Figure 5.

Please delete the sequence listing incorporated within the specification at pages 92 to 97 as follows:

~~SEQUENCE LISTING~~

~~<110> Pan, Yang~~

~~<120> NOVEL MOLECULES OF THE TANGO 93 RELATED PROTEIN FAMILY AND USES THEREOF~~

~~<130>~~

<160> 6

<170> FastSEQ for Windows Version 3.0

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<211> 1360
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (137)...(604)

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caaattttcc agccttgtct ttgcctaaaa tttcctgctg tttatttcaa aatagggtct   120
acatactgtg gagctc atg atg gtt ctg agt ggg gca cta tgc ttc cga atg   172
                   Met Met Val Leu Ser Gly Ala Leu Cys Phe Arg Met
                   1   5   10

aag gat tca gcc ttg aag gta ctg tat ctg cac aat aac cag ctg ctg   220
Lys Asp Ser Ala Leu Lys Val Leu Tyr Leu His Asn Asn Gln Leu Leu
        15   20   25

gct gga gga ctg cac gca gag aag gtc att aaa ggt gag gag atc agt   268
Ala Gly Gly Leu His Ala Glu Lys Val Ile Lys Gly Glu Glu Ile Ser
        30   35   40

gtt gtc cca aat cgg gca ctg gat gcc agt ctg tcc cct gtc atc ctg   316
Val Val Pro Asn Arg Ala Leu Asp Ala Ser Leu Ser Pro Val Ile Leu
    45   50   55   60

ggc gtt caa gga gga agc cag tgc cta tct tgt ggg aca gag aaa ggg   364
Gly Val Gln Gly Gly Ser Gln Cys Leu Ser Cys Gly Thr Glu Lys Gly
                65   70   75

cca att ctg aaa ctt gag cca gtg aac atc atg gag ctc tac ctc ggg   412
Pro Ile Leu Lys Leu Glu Pro Val Asn Ile Met Glu Leu Tyr Leu Gly
                80   85   90

gcc aag gaa tca aag agc ttc acc ttc tac cgg cgg gat atg ggt ctt   460
Ala Lys Glu Ser Lys Ser Phe Thr Phe Tyr Arg Arg Asp Met Gly Leu
        95   100   105

acc tcc agc ttc gaa tcc gct gcc tac cca ggc tgg ttc ctc tgc acc   508
Thr Ser Ser Phe Glu Ser Ala Ala Tyr Pro Gly Trp Phe Leu Cys Thr
        110   115   120

tca ccg gaa gct gac cag cct gtc agg ctc act cag atc cct gag gac   556
Ser Pro Glu Ala Asp Gln Pro Val Arg Leu Thr Gln Ile Pro Glu Asp
125   130   135   140

ccc gcc tgg gat gct ccc atc aca gac ttc tac ttt cag cag tgt gac   604
Pro Ala Trp Asp Ala Pro Ile Thr Asp Phe Tyr Phe Gln Gln Cys Asp
            145   150   155

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gatagaggat agagagacag aggagctcca cagtaggtgg cttactcctc tccttcccta    724
ctggactccc gcttctgacc taaggcacac agacactctc ttctcctgca tcccagtgct    784
ggtaaatctt ctggtatttg gagctcaatg tgtagattct ttcagattgg atggtactac    844
ctctggtgtg gaacccaata gaaaccacgt aggaccaaca aagagcaaca taaagattc     904
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gctggctggg ccctttccct caaccttct gacatctgca gcctctctca ttcttgcctt     1084
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aaaaaaaaaa aaaaaaaaaa aaaaacatg cggccg                               1360
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<213> Mus musculus
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            20                  25                  30
His Ala Glu Lys Val Ile Lys Gly Glu Glu Ile Ser Val Val Pro Asn
        35                  40                  45
Arg Ala Leu Asp Ala Ser Leu Ser Pro Val Ile Leu Gly Val Gln Gly
    50                  55                  60
Gly Ser Gln Cys Leu Ser Cys Gly Thr Glu Lys Gly Pro Ile Leu Lys
65                  70                  75                  80
Leu Glu Pro Val Asn Ile Met Glu Leu Tyr Leu Gly Ala Lys Glu Ser
                85                  90                  95
Lys Ser Phe Thr Phe Tyr Arg Arg Asp Met Gly Leu Thr Ser Ser Phe
            100                 105                 110
Glu Ser Ala Ala Tyr Pro Gly Trp Phe Leu Cys Thr Ser Pro Glu Ala
        115                 120                 125
Asp Gln Pro Val Arg Leu Thr Gln Ile Pro Glu Asp Pro Ala Trp Asp
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Ala Pro Ile Thr Asp Phe Tyr Phe Gln Gln Cys Asp
145                 150                 155
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<212> DNA
<213> Mus musculus
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gaggagatca gtgttgtccc aaatcgggca ctggatgcca gtctgtcccc tgtcatcctg    180
ggcgttcaag gaggaagcca gtgcctatct tgtgggacag agaaggggcc aattctgaaa    240
cttgagccag tgaacatcat ggagctctac ctcgggggca aggaatcaaa gagcttcacc    300
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```
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           <213> Homo sapiens

           <220>
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           <222> (57)...(521)


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                                                                     Met
                                                                      1


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Val Leu Ser Gly Ala Leu Cys Phe Arg Met Lys Asp Ser Ala Leu Lys
              5                    10                   15


gtg ctt tat ctg cat aat aac cag ctt cta gct gga ggg ctg cat gca          155
Val Leu Tyr Leu His Asn Asn Gln Leu Leu Ala Gly Gly Leu His Ala
          20                   25                   30


ggg aag gtc att aaa ggt gaa gag atc agc gtg gtc ccc aat cgg tgg          203
Gly Lys Val Ile Lys Gly Glu Glu Ile Ser Val Val Pro Asn Arg Trp
          35                   40                   45


ctg gat gcc agc ctg tcc ccc gtc atc ctg ggt gtc cag ggt gga agc          251
Leu Asp Ala Ser Leu Ser Pro Val Ile Leu Gly Val Gln Gly Gly Ser
      50                   55                   60                   65


cag tgc ctg tca tgt ggg gtg ggg cag gag ccg act cta aca cta gag          299
Gln Cys Leu Ser Cys Gly Val Gly Gln Glu Pro Thr Leu Thr Leu Glu
              70                   75                   80


cca gtg aac atc atg gag ctc tat ctt ggt gcc aag gaa tcc aag agc          347
Pro Val Asn Ile Met Glu Leu Tyr Leu Gly Ala Lys Glu Ser Lys Ser
              85                   90                   95


ttc acc ttc tac cgg cgg gac atg ggg ctc acc tcc agc ttc gag tcg          395
Phe Thr Phe Tyr Arg Arg Asp Met Gly Leu Thr Ser Ser Phe Glu Ser
          100                  105                  110


gct gcc tac ccg ggc tgg ttc ctg tgc acg gtg cct gaa gcc gat cag          443
Ala Ala Tyr Pro Gly Trp Phe Leu Cys Thr Val Pro Glu Ala Asp Gln
          115                  120                  125


cct gtc aga ctc acc cag ctt ccc gag aat ggt ggc tgg aat gcc ccc          491
Pro Val Arg Leu Thr Gln Leu Pro Glu Asn Gly Gly Trp Asn Ala Pro
      130                  135                  140                  145
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atc aca gac ttc tac ttc cag cag tgt gac tagggcaacg tgcccccag   541
Ile Thr Asp Phe Tyr Phe Gln Gln Cys Asp
                        150   155

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actgtcatat gctacctttc ctatctcttc cctcatcatc ttgttgtggg catgaggagg   1081
tggtgatgtc agaagaaatg gctcgagctc agaagataaa agataagtag ggtatgctga   1141
tcctcttta aaaacccaag atacaatcaa aatcccagat gctggtctct attcccatga   1201
aaaagtgctc atgacatatt gagaagacct acttacaaag tggcatatat tgcaatttat   1261
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gc   1323

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            20   25   30
Ala Gly Lys Val Ile Lys Gly Glu Glu Ile Ser Val Val Pro Asn Arg
        35   40   45
Trp Leu Asp Ala Ser Leu Ser Pro Val Ile Leu Gly Val Gln Gly Gly
    50   55   60
Ser Gln Cys Leu Ser Cys Gly Val Gly Gln Glu Pro Thr Leu Thr Leu
65   70   75   80
Glu Pro Val Asn Ile Met Glu Leu Tyr Leu Gly Ala Lys Glu Ser Lys
                85   90   95
Ser Phe Thr Phe Tyr Arg Arg Asp Met Gly Leu Thr Ser Ser Phe Glu
            100   105   110
Ser Ala Ala Tyr Pro Gly Trp Phe Leu Cys Thr Val Pro Glu Ala Asp
            115   120   125
Gln Pro Val Arg Leu Thr Gln Leu Pro Glu Asn Gly Gly Trp Asn Ala
        130   135   140
Pro Ile Thr Asp Phe Tyr Phe Gln Gln Cys Asp
145   150   155

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gagatcagcg tggtccccaa tcggtggctg gatgccagcc tgtcccccgt catcctgggt   180

~~gtccagggtg gaagccagtg cctgtcatgt ggggtggggc aggagccgac tctaacacta~~ ~~240~~
~~gagccagtga acatcatgga gctctatctt ggtgccaagg aatccaagag cttcaccttc~~ ~~300~~
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Please re-number pages 97 to 105 as pages 92 to 100